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TECH CENTER 1600/2900



1600

#10/ Raw
Sag
Listing

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/840,704A

DATE: 11/21/2002

TIME: 11:22:39

Input Set : F:\SEQLIST.txt

Output Set: N:\CRF4\11212002\I840704A.raw

4 <110> APPLICANT: Dedhar, Shoukat
5 Hannigan, Greg
7 <120> TITLE OF INVENTION: Integrin-Linked Kinase and its Uses
10 <130> FILE REFERENCE: KINE-001CON2
12 <140> CURRENT APPLICATION NUMBER: US 09/840,704A
13 <141> CURRENT FILING DATE: 2001-04-23
15 <150> PRIOR APPLICATION NUMBER: 60/009,074
16 <151> PRIOR FILING DATE: 1995-12-21
18 <150> PRIOR APPLICATION NUMBER: 08/752,345
19 <151> PRIOR FILING DATE: 1996-11-19
21 <150> PRIOR APPLICATION NUMBER: 08/955,841
22 <151> PRIOR FILING DATE: 1997-10-21
24 <150> PRIOR APPLICATION NUMBER: 09/390,425
25 <151> PRIOR FILING DATE: 1999-09-03
27 <150> PRIOR APPLICATION NUMBER: 09/566,906
28 <151> PRIOR FILING DATE: 2000-05-09
30 <160> NUMBER OF SEQ ID NOS: 21
32 <170> SOFTWARE: FastSEQ for Windows Version 4.0
34 <210> SEQ ID NO: 1
35 <211> LENGTH: 1789
36 <212> TYPE: DNA
37 <213> ORGANISM: Homo sapiens
39 <220> FEATURE:
40 <221> NAME/KEY: CDS
41 <222> LOCATION: (157)...(1512)
W--> 43 <221> NAME/KEY: Other
44 <222> LOCATION: (0)...(0)

W--> 46 <400> 1

47 gaattcatct gtcgactgct accacgggag ttccccggag aaggatcctg cagcccgagt 60
48 cccgaggata aagcttgggg ttcatactcc ttccctggat cactccacag tcctcaggct 120
49 tccccaatcc aggggactcg gcgccgggac gctgct atg gac gac att ttc act 174
50 Met Asp Asp Ile Phe Thr
51 1 5
53 cag tgc cgg gag ggc aac gca gtc gcc gtt cgc ctg tgg ctg gac aac 222
54 Gln Cys Arg Glu Gly Asn Ala Val Ala Val Arg Leu Trp Leu Asp Asn
55 10 15 20
57 acg gag aac gac ctc aac cag ggg gac gat cat ggc ttc tcc ccc ttg 270
58 Thr Glu Asn Asp Leu Asn Gln Gly Asp Asp His Gly Phe Ser Pro Leu
59 25 30 35
61 cac tgg gcc tgc cga gag ggc cgc tct gct gtg gtt gag atg ttg atc 318
62 His Trp Ala Cys Arg Glu Gly Arg Ser Ala Val Val Glu Met Leu Ile
63 40 45 50
65 atg cgg ggg gca cgg atc aat gta atg aac cgt ggg gat gac acc ccc 366

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66 Met Arg Gly Ala Arg Ile Asn Val Met Asn Arg Gly Asp Asp Thr Pro
67 55 60 65 70
69 ctg cat ctg gca gcc agt cat gga cac cgt gat att gta cag aag cta 414
70 Leu His Leu Ala Ala Ser His Gly His Arg Asp Ile Val Gln Lys Leu
71 75 80 85
73 ttg cag tac aag gca gac atc aat gca gtg aat gaa cac ggg aat gtg 462
74 Leu Gln Tyr Lys Ala Asp Ile Asn Ala Val Asn Glu His Gly Asn Val
75 90 95 100
77 ccc ctg cac tat gcc tgt ttt tgg ggc caa gat caa gtg gca gag gac 510
78 Pro Leu His Tyr Ala Cys Phe Trp Gly Gln Asp Gln Val Ala Glu Asp
79 105 110 115
81 ctg gtg gca aat ggg gcc ctt gtc agc atc tgt aac aag tat gga gag 558
82 Leu Val Ala Asn Gly Ala Leu Val Ser Ile Cys Asn Lys Tyr Gly Glu
83 120 125 130
85 atg cct gtg gac aaa gcc aag gca ccc ctg aga gag ctt ctc cga gag 606
86 Met Pro Val Asp Lys Ala Lys Ala Pro Leu Arg Glu Leu Leu Arg Glu
87 135 140 145 150
89 cgg gca gag aag atg ggc cag aat ctc aac cgt att cca tac aag gac 654
90 Arg Ala Glu Lys Met Gly Gln Asn Leu Asn Arg Ile Pro Tyr Lys Asp
91 155 160 165
93 aca ttc tgg aag ggg acc acc cgc act cgg ccc cga aat gga acc ctg 702
94 Thr Phe Trp Lys Gly Thr Thr Arg Thr Arg Pro Arg Asn Gly Thr Leu
95 170 175 180
97 aac aaa cac tct ggc att gac ttc aaa cag ctt aac ttc ctg acg aag 750
98 Asn Lys His Ser Gly Ile Asp Phe Lys Gln Leu Asn Phe Leu Thr Lys
99 185 190 195
101 ctc aac gag aat cac tct gga gag cta tgg aag ggc cgc tgg cag ggc 798
102 Leu Asn Glu Asn His Ser Gly Glu Leu Trp Lys Gly Arg Trp Gln Gly
103 200 205 210
105 aat gac att gtc gtg aag gtg ctg aag gtt cga gac tgg agt aca agg 846
106 Asn Asp Ile Val Val Lys Val Leu Lys Val Arg Asp Trp Ser Thr Arg
107 215 220 225 230
109 aag agc agg gac ttc aat gaa gag tgt ccc cgg ctc agg att ttc tcg 894
110 Lys Ser Arg Asp Phe Asn Glu Glu Cys Pro Arg Leu Arg Ile Phe Ser
111 235 240 245
113 cat cca aat gtg ctc cca gtg cta ggt gcc tgc cag tct cca cct gct 942
114 His Pro Asn Val Leu Pro Val Leu Gly Ala Cys Gln Ser Pro Pro Ala
115 250 255 260
117 cct cat cct act ctc atc aca cac tgg atg ccg tat gga tcc ctc tac 990
118 Pro His Pro Thr Leu Ile Thr His Trp Met Pro Tyr Gly Ser Leu Tyr
119 265 270 275
121 aat gta cta cat gaa ggc acc aat ttc gtc gtg gac cag agc cag gct 1038
122 Asn Val Leu His Glu Gly Thr Asn Phe Val Val Asp Gln Ser Gln Ala
123 280 285 290
125 gtg aag ttt gct ttg gac atg gca agg ggc atg gcc ttc cta cac aca 1086
126 Val Lys Phe Ala Leu Asp Met Ala Arg Gly Met Ala Phe Leu His Thr
127 295 300 305 310
129 cta gag ccc ctc atc cca cga cat gca ctc aat agc cgt agt gta atg 1134
130 Leu Glu Pro Leu Ile Pro Arg His Ala Leu Asn Ser Arg Ser Val Met

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131          315          320          325
133 att gat gag gac atg act gcc cga att agc atg gct gat gtc aag ttc      1182
134 Ile Asp Glu Asp Met Thr Ala Arg Ile Ser Met Ala Asp Val Lys Phe
135          330          335          340
137 tct ttc caa tgt cct ggt cgc atg tat gca cct gcc tgg gta gcc ccc      1230
138 Ser Phe Gln Cys Pro Gly Arg Met Tyr Ala Pro Ala Trp Val Ala Pro
139          345          350          355
141 gaa gct ctg cag aag aag cct gaa gac aca aac aga cgc tca gca gac      1278
142 Glu Ala Leu Gln Lys Lys Pro Glu Asp Thr Asn Arg Arg Ser Ala Asp
143          360          365          370
145 atg tgg agt ttt gca gtg ctt ctg tgg gaa ctg gtg aca cgg gag gta      1326
146 Met Trp Ser Phe Ala Val Leu Leu Trp Glu Leu Val Thr Arg Glu Val
147 375          380          385          390
149 ccc ttt gct gac ctc tcc aat atg gag att gga atg aag gtg gca ttg      1374
150 Pro Phe Ala Asp Leu Ser Asn Met Glu Ile Gly Met Lys Val Ala Leu
151          395          400          405
153 gaa ggc ctt cgg cct acc atc cca cca ggt att tcc cct cat gtg tgt      1422
154 Glu Gly Leu Arg Pro Thr Ile Pro Pro Gly Ile Ser Pro His Val Cys
155          410          415          420
157 aag ctc atg aag atc tgc atg aat gaa gac cct gca aag cga ccc aaa      1470
158 Lys Leu Met Lys Ile Cys Met Asn Glu Asp Pro Ala Lys Arg Pro Lys
159          425          430          435
161 ttt gac atg att gtg cct atc ctt gag aag atg cag gac aag      1512
162 Phe Asp Met Ile Val Pro Ile Leu Glu Lys Met Gln Asp Lys
163          440          445          450
165 taggactgga aggtccttgc ctgaactcca gaggtgtcgg gacatgggtg ggggaatgca      1572
166 cctcccaaaa gcagcaggcc tctggttgcc tccccgcct ccagtcatgg tactaccca      1632
167 gcttggtgac catcccttc ccccatccct accactgtgc gcaagagggg cgggctcaga      1692
168 gctttgtcac ttgccacatg gtgtctccca acatgggagg gatcagcccc gcctgtcaca      1752
169 ataaagttaa ttatgaaaaa aaaaaaaaaa aaaaaaa      1789
171 <210> SEQ ID NO: 2
172 <211> LENGTH: 452
173 <212> TYPE: PRT
174 <213> ORGANISM: Homo sapiens
176 <400> SEQUENCE: 2
177 Met Asp Asp Ile Phe Thr Gln Cys Arg Glu Gly Asn Ala Val Ala Val
178 1          5          10          15
179 Arg Leu Trp Leu Asp Asn Thr Glu Asn Asp Leu Asn Gln Gly Asp Asp
180          20          25          30
181 His Gly Phe Ser Pro Leu His Trp Ala Cys Arg Glu Gly Arg Ser Ala
182          35          40          45
183 Val Val Glu Met Leu Ile Met Arg Gly Ala Arg Ile Asn Val Met Asn
184          50          55          60
185 Arg Gly Asp Asp Thr Pro Leu His Leu Ala Ala Ser His Gly His Arg
186 65          70          75          80
187 Asp Ile Val Gln Lys Leu Leu Gln Tyr Lys Ala Asp Ile Asn Ala Val
188          85          90          95
189 Asn Glu His Gly Asn Val Pro Leu His Tyr Ala Cys Phe Trp Gly Gln
190          100          105          110

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191 Asp Gln Val Ala Glu Asp Leu Val Ala Asn Gly Ala Leu Val Ser Ile
192      115      120      125
193 Cys Asn Lys Tyr Gly Glu Met Pro Val Asp Lys Ala Lys Ala Pro Leu
194      130      135      140
195 Arg Glu Leu Leu Arg Glu Arg Ala Glu Lys Met Gly Gln Asn Leu Asn
196 145      150      155      160
197 Arg Ile Pro Tyr Lys Asp Thr Phe Trp Lys Gly Thr Thr Arg Thr Arg
198      165      170      175
199 Pro Arg Asn Gly Thr Leu Asn Lys His Ser Gly Ile Asp Phe Lys Gln
200      180      185      190
201 Leu Asn Phe Leu Thr Lys Leu Asn Glu Asn His Ser Gly Glu Leu Trp
202      195      200      205
203 Lys Gly Arg Trp Gln Gly Asn Asp Ile Val Val Lys Val Leu Lys Val
204      210      215      220
205 Arg Asp Trp Ser Thr Arg Lys Ser Arg Asp Phe Asn Glu Glu Cys Pro
206 225      230      235      240
207 Arg Leu Arg Ile Phe Ser His Pro Asn Val Leu Pro Val Leu Gly Ala
208      245      250      255
209 Cys Gln Ser Pro Pro Ala Pro His Pro Thr Leu Ile Thr His Trp Met
210      260      265      270
211 Pro Tyr Gly Ser Leu Tyr Asn Val Leu His Glu Gly Thr Asn Phe Val
212      275      280      285
213 Val Asp Gln Ser Gln Ala Val Lys Phe Ala Leu Asp Met Ala Arg Gly
214      290      295      300
215 Met Ala Phe Leu His Thr Leu Glu Pro Leu Ile Pro Arg His Ala Leu
216 305      310      315      320
217 Asn Ser Arg Ser Val Met Ile Asp Glu Asp Met Thr Ala Arg Ile Ser
218      325      330      335
219 Met Ala Asp Val Lys Phe Ser Phe Gln Cys Pro Gly Arg Met Tyr Ala
220      340      345      350
221 Pro Ala Trp Val Ala Pro Glu Ala Leu Gln Lys Lys Pro Glu Asp Thr
222      355      360      365
223 Asn Arg Arg Ser Ala Asp Met Trp Ser Phe Ala Val Leu Leu Trp Glu
224      370      375      380
225 Leu Val Thr Arg Glu Val Pro Phe Ala Asp Leu Ser Asn Met Glu Ile
226 385      390      395      400
227 Gly Met Lys Val Ala Leu Glu Gly Leu Arg Pro Thr Ile Pro Pro Gly
228      405      410      415
229 Ile Ser Pro His Val Cys Lys Leu Met Lys Ile Cys Met Asn Glu Asp
230      420      425      430
231 Pro Ala Lys Arg Pro Lys Phe Asp Met Ile Val Pro Ile Leu Glu Lys
232      435      440      445
233 Met Gln Asp Lys
234      450
237 <210> SEQ ID NO: 3
238 <211> LENGTH: 452
239 <212> TYPE: PRT
240 <213> ORGANISM: Homo sapiens
242 <220> FEATURE:

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W--> 243 <221> NAME/KEY: Other

244 <222> LOCATION: (0)...(0)

246 <400> SEQUENCE: 3

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247 Met Asp Asp Ile Phe Thr Gln Cys Arg Glu Gly Asn Ala Val Ala Val
248   1           5           10           15
249 Arg Leu Trp Leu Asp Asn Thr Glu Asn Asp Leu Asn Gln Gly Asp Asp
250           20           25           30
251 His Gly Phe Ser Pro Leu His Trp Ala Cys Arg Glu Gly Arg Ser Ala
252           35           40           45
253 Val Val Glu Met Leu Ile Met Arg Gly Ala Arg Ile Asn Val Met Asn
254   50           55           60
255 Arg Gly Asp Asp Thr Pro Leu His Leu Ala Ala Ser His Gly His Arg
256 65           70           75           80
257 Asp Ile Val Gln Lys Leu Leu Gln Tyr Lys Ala Asp Ile Asn Ala Val
258           85           90           95
259 Asn Glu His Gly Asn Val Pro Leu His Tyr Ala Cys Phe Trp Gly Gln
260           100          105          110
261 Asp Gln Val Ala Glu Asp Leu Val Ala Asn Gly Ala Leu Val Ser Ile
262           115          120          125
263 Cys Asn Lys Tyr Gly Glu Met Pro Val Asp Lys Ala Lys Ala Pro Leu
264   130          135          140
265 Arg Glu Leu Leu Arg Glu Arg Ala Glu Lys Met Gly Gln Asn Leu Asn
266 145          150          155          160
267 Arg Ile Pro Tyr Lys Asp Thr Phe Trp Lys Gly Thr Thr Arg Thr Arg
268           165          170          175
269 Pro Arg Asn Gly Thr Leu Asn Lys His Ser Gly Ile Asp Phe Lys Gln
270           180          185          190
271 Leu Asn Phe Leu Thr Lys Leu Asn Glu Asn His Ser Gly Glu Leu Trp
272   195          200          205
273 Lys Gly Arg Trp Gln Gly Asn Asp Ile Val Val Lys Val Leu Lys Val
274   210          215          220
275 Arg Asp Trp Ser Thr Arg Lys Ser Arg Asp Phe Asn Glu Glu Cys Pro
276 225          230          235          240
277 Arg Leu Arg Ile Phe Ser His Pro Asn Val Leu Pro Val Leu Gly Ala
278           245          250          255
279 Cys Gln Ser Pro Pro Ala Pro His Pro Thr Leu Ile Thr His Trp Met
280           260          265          270
281 Pro Tyr Gly Ser Leu Tyr Asn Val Leu His Glu Gly Thr Asn Phe Val
282           275          280          285
283 Val Asp Gln Ser Gln Ala Val Lys Phe Ala Leu Asp Met Ala Arg Gly
284   290          295          300
285 Met Ala Phe Leu His Thr Leu Glu Pro Leu Ile Pro Arg His Ala Leu
286 305          310          315          320
287 Asn Ser Arg Ser Val Met Ile Asp Glu Asp Met Thr Ala Arg Ile Ser
288           325          330          335
289 Met Ala Asp Val Lys Phe Ser Phe Gln Cys Pro Gly Arg Met Tyr Ala
290           340          345          350
291 Pro Ala Trp Val Ala Pro Glu Ala Leu Gln Lys Lys Pro Glu Asp Thr
292           355          360          365

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 11/21/2002
PATENT APPLICATION: US/09/840,704A TIME: 11:22:40

Input Set : F:\SEQLIST.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:14; Xaa Pos. 2,4,5

Seq#:17; Xaa Pos. 10,15